

09036544.041701

1 GGGGATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT  
51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT  
101 CAGGACCGG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG  
151 GCCAECACCTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG  
251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA  
301 CGGGGGGTTT GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA  
351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG  
401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGTCGGA ACAGGAGAGC  
451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GTATCTTTA TAGTCCTGTC  
501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG  
551 GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCCGAATTA CCGCGGTCTT  
601 TCTCAACGTA AACTTTTACA GCGGCGCGTC ATTTGATATG ATGCGCCCCG  
651 CTTCCCGATA AGGGAGCAGG CCAGTAAAAG CATTACCCGT GGTGGGGTTC  
701 CCCAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTCAT CGACTTCGAA  
751 GGTTGGAATC CTTCCCCAC CACCATCACT TTCAAAGTC CGAAAGAATC  
801 TGCTCCCTGC TTGTGTGTG GAGGTCGCTG AGTAGTGGC GAGTAAAT  
851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT  
901 TAGGGTTAGG CGTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACGC  
951 GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA  
1001 TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAA  
1051 TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATG ACGTCAATA  
1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA  
1151 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA  
1201 TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC  
1251 CCTGGCATTG TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG  
1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA  
1351 GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC  
1401 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACC AATCAACGG  
1451 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG  
1501 AATTCCTGGG CGGGACTGGG GAGTGGCGAG CCTCAGATG CTGCATATA  
1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG  
1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAA GCCTCAATA  
1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGA TCTTCCATAC CTACCAGTTC

FIG. 1-1

Cont  
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1701 TGGCCTGCA GGTGCGGCC GCGACTCTAG AGGATCTTTG TGAAGGAACC  
1751 TTAATTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA  
1801 GCTCTAAGGT AAATATAAAA TTTTAAAGTG TATAATGTGT TAACTACTG  
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG  
1901 GGAGCAGTGG TGAATGCCT TTAATGAGGA AAACCTGTTT TGCTCAGAAG  
1951 AAATGCCATC TAGTGATGAT GAGGCTACTG CTGACTCTCA ACATTCTACT  
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCTTCAGA  
2051 ATTGCTAAGT TTTTGTAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT  
2101 GCTTTGCTAT TTACACCACA AAGGAAAAAG CTGCACTGCT ATACAAGAAA  
2151 ATTATGGAAA AATATTCTGT AACCTTTATA AGTAGGCATA ACAGTTATAA  
2201 TCATAACATA CTGTTTTTTC TTAATCCACA CAGGCATAGA GTGTCTGCTA  
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTTT AATTTGTAAA  
2301 GGGGTTAATA AGGAATATTT CATGTATAGT GCCTTGACTA GAGATCATAA  
2351 TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA AAACCTCCCA  
2401 CACCTCCCCC TGAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTAA  
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA  
2501 ATTTACAAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTC  
2551 AAATCATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA  
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA  
2651 GCATGCATCT CAATFAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC  
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT  
2751 AGTCCCGCCC CTAATCCGC CCATCCCGCC CCTAATCCG CCCAGTCCG  
2801 CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTATTTA TGCAGAGGCC  
2851 GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT  
2901 TGGAGGCCTA GGCTTTTGCA AAAAGCTAAT TC

FIG. 1-2

[illegible]

FIG. 2-1

Cont  
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300 CAAGTTCACCAGCAGAAAGGCCCGCCCCTCCCCAGACCTCGAGTTCAGCCAAAACCTCCC (1020)  
GLNVALHISGLNGLNLYSGLYPROPROLEUPROARGPROARGVALGLNPROLYSPROPRO  
320 CATGGGGCAGCAGAAAACCTCATTGTCCCCCTCCTCTAATTAAAAAGATAGAAACTGTCT (1080)  
HISGLYALAALAGLUASNSEUSERPROSEUSERASNE  
TTTTCAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCATATCCGTACTTCCATG (1140)  
AGGTGTTTTCTGTGTGCAGAACATTGTCACTCCTGAGGCTGTGGGCCACAGCCACCTCT (1200)  
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTGGTCTCCTCAGAGAGCTC (1260)  
CATCACACCAGTAAGGAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGC (1320)  
ACAGAAATCTTAGAGATTTCTTGTCCTCTCAGGTCATGTGTAGATGCGATAAATCAAG (1380)  
TGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTT (1440)  
CTTATGTGCCCTGGTGGACACTTGCCACCATCCTGTGAGTAAAAGTGAAATAAAAGCTT (1500)  
TGAC (1504)

FIG. 2-2

**Figure 1**

1 G C C C C A C G A G C C A T G G T T G C T G G A G C G A C G C G G G G C C T G G G G T C C T C A G C G T G G T C I G C C I G C A C T G C T T T G G T T T C A T C 90  
MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLeuSerValValCysLeuLeuIleCysPheGlyPheIle 26

91 A G C T G T T T T C C C A A C A A A T A T A T G G T G T T G T G T A T G G G A A T G T A A C T T C C A T G T A C C A A G C A A T G T G C C T T T A A A A G A G G T C C T A T G G 180  
27 SerCysPheSerGlnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisValProSerAsnValProLeuLysGluValLeuTrp 56  
---CH0---

181 A A A A A C A A A A G G A T A A A G T T G C A G A A C T G G A A A T T C T G A A T T C A G A G C T T T C T C A T C T T T A A A A T A G G G T T A T T A T T I A G A C A C T G T G 270  
57 LysLysGlnLysAspLysValAlaGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLysAsnArgValTyrLeuAspThrVal 86

271 T C A G G T A G C C T C A C T A T C T A C A A C T T A A C A T C A T C A G A T G A G A T G A G A T G A A A T G G A A T C G C C A A A T A T T A C T G A T A C C A I G A A G T T C 360  
87 SerGlySerLeuThrIleTyrAsnLeuThrSerSerAspGluAspGluTyrGluMetGluSerProAsnIleThrAspThrMetLysPhe 116  
---CH0---

361 T T T C T T A T G T G C T T G A G T C T C T C C A T C T C C C A C A C T A A C T T G T G C A T T G A C T A A T G G A A G C A T T G A A G T C C A A T G C A T G A T A C C A G A G 450  
117 PheLeuTyrValLeuGluSerLeuProSerProThrLeuThrCysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleProGlu 146  
---CH0---

451 C A T T A C A A C A G C C A T C G A G G A C T T A T A A T G T A C T A T C A T G G A T T G T C C T A T G G A G C A A T G T A A A C G T A A C T C A A C C A G T A T A T A T T T T A A G 540  
147 HisTyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCysProMetGluGlnCysLysArgAsnSerThrSerIleTyrPheLys 176  
---CH0---

541 A T G G A A A A T G A T C T T C C A C A A A A A A T A C A G T G T A C T C T T A G C A A T C C A T T A T T A A T A C A A C A T C A T C A A T C A T T T T G A C A A C C T G T A T C 630  
177 MetGluAsnAspLeuProGlnLysIleGlnCysThrLeuSerAsnProLeuPheAsnThrThrSerSerIleIleLeuThrThrCysIle 206  
---CH0---

631 C C A A G C A G C G G T C A T T C A A G A C A C A G A T A T G C A C T T A T A C C C A T A C C A T T A G C A G T A A T T A C A A C A T G T A T T G T G C T G T A T A T G A A T G T T 720  
207 ProSerSerGlyHisSerArgHisArgTyrAlaLeuIleProIleProLeuAlaValIleThrThrCysIleValIleValIleTyrMetAsnVal 236  
=====

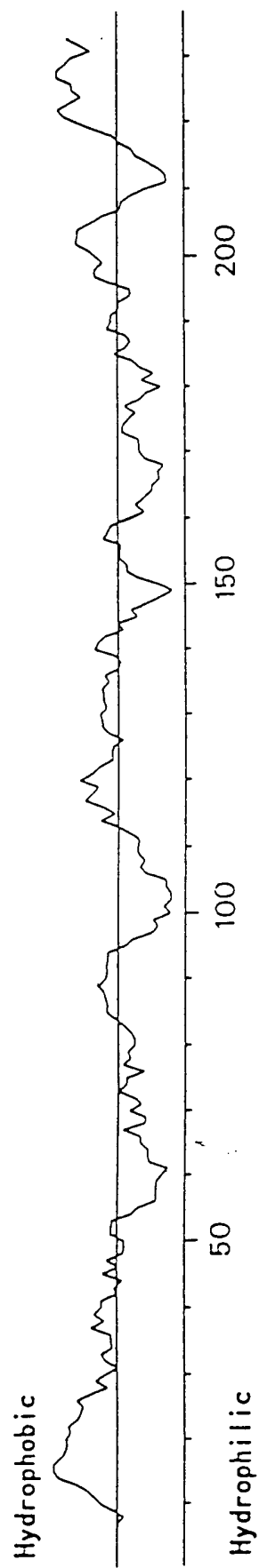
721 C T T T A A T T G A G A A G A C A A T T T C T T C A T T T T T A G G T A T T C I G A A A T G T G A C A G A A A A C C A G A C A G A C C A A C T C C A A T T G A T T G G T A A C A G 810  
237 LeuEnd  
==

811 A A G A T G A A G A C A A C A G C A T A A C T A A A T A T T T T A A A A A C T A A A A A G C C A T C T G A T T T C T C A T T T 874

FIG. 4A

FIG. 4A

FIG. 4B



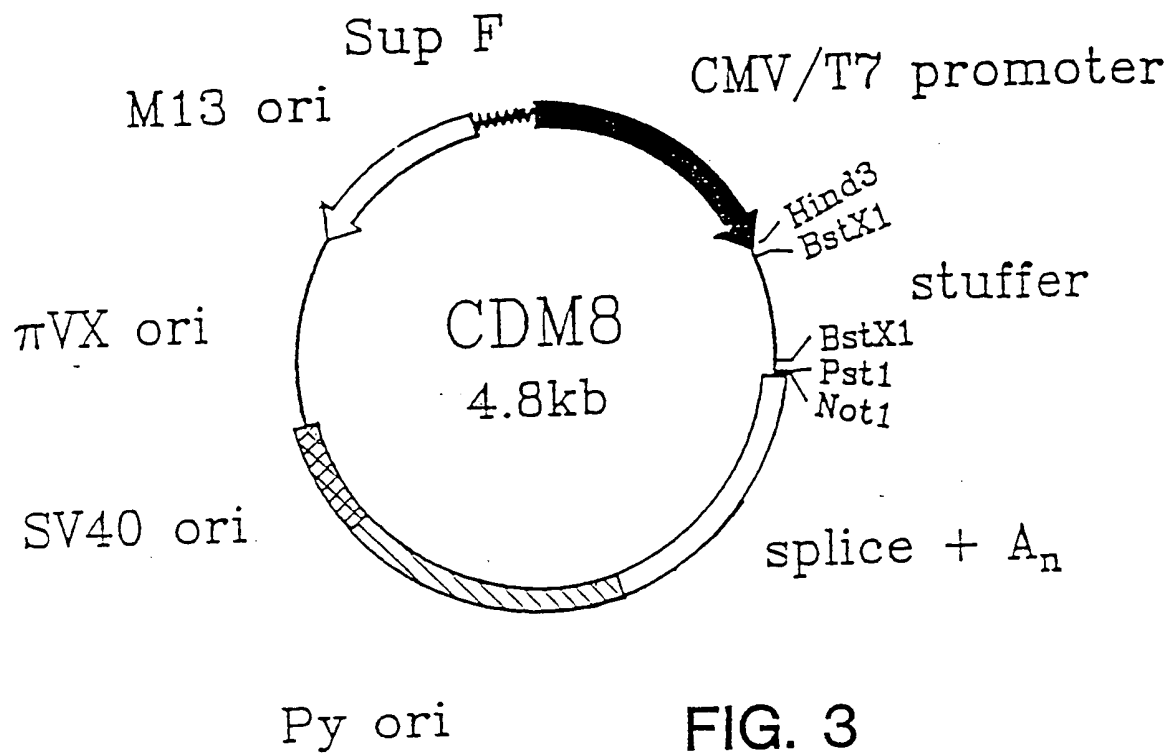


FIG. 3

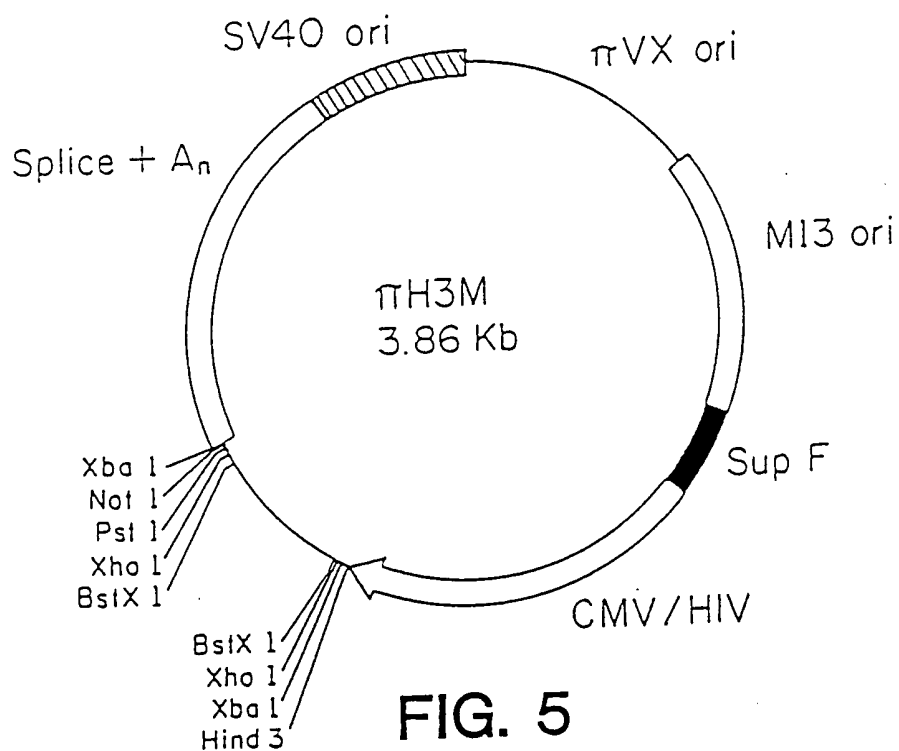


FIG. 5

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1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGTGGT  
 51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAAGTGGCT  
 101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA  
 151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT  
 201 AATCCTGTGA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG  
 251 GGTGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA  
 301 ACGGGGGGTT CGTGACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA  
 351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG  
 401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG  
 451 CGCACCAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT  
 501 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG  
 551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT  
 601 AGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT  
 651 AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT  
 701 AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTGTTC CAGTTTGGAA  
 751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA  
 801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA  
 851 AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG  
 901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA  
 951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA  
 1001 GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA ATGCGCCGCT  
 1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCTTTCC

FIG. 6-1



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1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTTT  
1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTTC TCAACGTAAC  
1201 ACTTTACAGC GGCGCGTCAT TTGATATGAT GCGCCCCGCT TCCCGATAAG  
1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGGTTCCC GAGCGGCCAA  
1301 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG TTCGAATCCT  
1351 TCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCTGCTT  
1401 GTGTGTTGGA GGTCGCTGAG TAGTGCGCGA GTAAAATTTA AGCTACAACA  
1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG  
1501 TTTTGCGCTG CTTGCGGATG TACGGGCCAG ATATACGCGT TGACATTGAT  
1551 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC  
1601 CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCCCGCCTGG  
1651 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTC  
1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT  
1751 TTACGGTAAAT CTGCCCACTT GGCAGTACAT CAAGTGATC ATATGCCAAG  
1801 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCCG TGGCATTATG  
1851 CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA CATCTACGTA  
1901 TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG  
1951 GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATG  
2001 ACGTCAATGG GAGTTTGTTT TGGCACCAAA ATCAACGGGA CTTTCCAAAA  
2051 TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGAA TTCCTGGGCG  
2101 GGA CTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT  
2151 TGCCTGTACT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT  
2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCAATAAAG CTTCTAGAGA  
2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

FIG. 6-2

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTC AAGCATGACA  
2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTGAACGA  
2401 GGTGGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGGG  
2451 TTCAGCAGCC GCGCTTTTAC TGGCACTTCA GGAACAAGCG GCGCTGCTC  
2501 GACGCACTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTGGTGCC  
2551 GAGAGCCGAC GACGACTGGC GCTCATTTCT GACTGGGAAT GCGCGCAGCT  
2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC  
2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGCCGC GACTCTAGAG  
2701 GATCTTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC  
2751 TACCTACAGA GATTTAAAGC TCTAAGGTAA ATATAAAATT TTAAAGTGTA  
2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC  
2851 CTATGGAAC- GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA  
2901 ACCTGTTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT  
2951 GACTCTCAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC  
3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTTA  
3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GAAAAAGCT  
3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG  
3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTCTT ACTCCACACA  
3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT  
3251 AGCTTTTTAA TTTGTAAAGG GGTTAATAAG GAATATTTGA TGTATAGTGC  
3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTTGTAGA GGTTTTACTT  
3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAATGAA  
3401 TGCAATTGTT GTTGTTAACT TGTTTATTGC AGCTTATAAT GGTTACAAAT  
3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TCACTGCAT

FIG. 6-3

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3501 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT  
3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG  
3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT  
3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT  
3701 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC  
3751 TAACTCCGCC CAGTTCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT  
3801 TTTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA  
3851 GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTTCAGAA AAGCTAATTC

FIG. 6-4

AGACTCTCAGGCCTTGGCAGGTGCGTCTTTCAGTTCCTCCCTCACACTTCGGGTTCTCGGG (60)  
 GAGGAGGGGCTGGAACCCTAGCCCATCGTCAGGACAAAGATGCTCAGGCTGCTCTTGGCT (120)  
 METLEUARGLEULEULEUALA  
 -18  
 CTCAACTTAATCCCTTCAATCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCC (180)  
 LEUASNLEUPHEPROSERILEGLNVALTHRGLYASNLYSILELEUVALLYSGLNSEPRO  
 +1  
 10 ATGCTTGTAAGGTACGACAATGCGGTCAAACCTTAGCTGCAAGTATTCCTACAATCTCTC (240)  
 METLEUVALALATYRASPASNALVALASNLEUSERCYSLYSTYRSERTYRASNLEUPHE  
 ---CHO---  
 30 TCAAGGGAGTTCGGGCATCCCTTCACAAAGGACTGGATAGTGCTGTGGAGTCTGTGT (300)  
 SERARGGLUPHEARGALASERLEUHISLYSGLYLEUASPSEALVALGLUVALCYSVAL  
 GTATATGGGAATTACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTTCAACTGTGAT (360)  
 50 VALTYRGLYASNLYSERGLNGLNLEUGLNVALTYRSERLYSTHRGLYPHEASNLYSASP  
 ---CHO---  
 70 GGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGAAATTTGTATGTTAACCAAAC (420)  
 GLYLYSLEUGLYASNGLUSERVALTHRPHETYLEUGLNASNLEUTYRVALASNLNTHR  
 ---CHO---  
 90 GATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAG (480)  
 ASPILETYRPHECYSLYSILEGLUVALMETTYRPROPROTYRLEUASPASNGLULYS  
 AGCAATGGAACCATTATCCATGTGAAAGGAAACACCTTTGTCCAAGTCCCCTATTTCC (540)  
 110 SERASNGLYTHRILEILEHISVALLYSGLYLYSHISLEUCYSPROSERPROLEUPHEPRO  
 ---CHO---  
 130 GGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTGGTGGAGTCCTGGCTTGCTATAGC (600)  
 GLYPROSERLYSPROPHETRPVALLEUVALVALVALGLYGLYVALLEUALACYSTYRSE  
 -----TM-----  
 150 TTGCTAGTAACAGTGGCCTTTATTATTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCCTG (660)  
 LEULEUVALTHRVALALAPHEILEILEPHETRPVALARGSERLYSARGSERARGLEULEU  
 -----  
 170 CACAGTGACTACATGAACATGACTCCCCGCCGCCCGGGCCACCCGCAAGCATTACCA (720)  
 HISSERASPTYRMETASNMETTHRPROARGARGPROGLYPROTHRARGLYSHISTYRGLN  
 CCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAG (780)  
 190 PROTYRALAPROPROARGASPPHEALAALATYRARGSEREND  
 202  
 AGCCAGCCGGCTGGCAGCCCCCATCTGCTCAATATCACTGCTCTGGATAAGAAATGACC (840)  
 CCATCTCCAAGCCGCCACCTCAGCCCCCTGTGGGCCACCAATGCCAATTTTCTCGAGTG (900)  
 ACTAGACCAATATCAAGATCATTTTGAGACTCTGAAATGAAGTAAAGAGATTTCTGT (960)  
 GACAGGCCAAGTCTTACAGTGCCATGGCCACATTCAAACCTTACCATGTACTTAGTGACT (1020)  
 TGACTGAGAAGTTAGGGTAGAAAACAAAAAGGGAGTGGAATCTGGGAGCCTCTCCCTTT (1080)

FIG. 7-1

CTCACTCACCTGCACATCTCAGTCAAGCAAGTGTGGTATCCACAGACATTTAGTTGCÄ (1140)  
 GAAGAAAGGCTAGGAAATCÄTTCCTTTTGGTAAATGGGTGTTAATCTTTGGTAGTG (1200)  
 GGTAAACGGGGTAAGTTAGAGTAGGGGGAGGGATAGGAAGACATATTTAAAAACCATTÄ (1260)  
 AAACACTGTCTCCCACTCAAGAAATGAGCCACGTAGTTCCTATTTAATGCTGTTTCCTT (1320)  
 TAGTTTAGAAATACATAGACÄTTGTCTTTTATGAATTCTGATCATATTTAGTCATTTTGÄ (1380)  
 CCAAATGAGGGATTTGGTCÄAATGAGGGAÄTCCCTCAAAGCAATATCAGGTAAACCAAGT (1440)  
 TGCTTTCCTCACTCCCTGTCAATGAGACTTCAGTGTTAATGTTCACAATAACTTTCGAAÄ (1500)  
 GAATAAAATÄGTTC (1514)

FIG. 7-2

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TAGACCCAGAGAGGCTCAGCTGCACTCGCCCGGCTGGGAGAGCTGGGTGTGGGGAACATG (60)  
 MET  
 GCCGGGCTCCGAGGCTCCTGCTGCTGCCCTGCTTCTGGCGCTGGCTCGCGGCTGCCT (120)  
 ALAGLYPROPROARGLEULEULEULEUPROLEULEULEUALALEUALAARGGLYLEUPRO  
 GGGGCCCTGGCTGCCAAGGTAAGAGCTTCCCAGGCTCTCCATGGCCACAGCTCCGGAGC (180)  
 GLYALALEUALAALAGLN /  
 TCTCCCTGCCCATGAGCTCAGAGCCCCAGTCTGAGCCACAGCACAGCCCCAGGAAGC (240)  
 GGGTGGGTGCTGAGCGGCTCCAGTGTCTGAGGACTCATTTAAGAGAAGGAAAAAGGGT (300)  
 GGACCCGGTGGGAGTGGCCGGGGCTGTCCAGGCAGGGCCGCTGCTTTGGGAGGAAGAAG (360)  
 CCCACAGTCTCGGAACACGAGGACAGCACCTCCCCAACACCACAGCCGTGCCAGATC (420)  
 TGCTCCATGCCCCGTAAGGACCGTGTCTTTGGCGACATGTCAGCCCTGGGCTGTCTCAG (480)  
 GGCCCCACCATCCCCACCACTGTCCCCTGAGGGAGGACATTCTGTCTCTTCTGGCCA (540)  
 ACTGATGGTGACAGCCAGGTCTCCCAGAGGTGAGGAGTCTCCCCACTGCACGACTGT (600)  
 GLUVALGLNGLNSERPROHISCYSTHRTHRVA  
 CCCCGTGGGAGCCTCCGTCAACATCACCTGCTCCACCAGCGGGGCTGCGTGGGATCTA (660)  
 LPROVALGLYALASERVALASNILETHRCYSSERTHRSEGLYGLYLEUARGLYLETY  
 ---CHO---  
 CCTGAGGCAGCTCGGGCCACAGCCCCAAGACATCATTTACTACGAGGACGGGTGGTGCC (720)  
 RLEUARGLNLEUGLYPROGLNPROGLNASPILEILETYRTYRGLUASPGLYVALVALPR  
 CACTACGGAACAGCGTTCCGGGGCCGATCGACTTCTCAGGGTCCCAGGACAACCTGAC (780)  
 OTHRTHRASPARGARGPHEARGGLYARGILEASPPHESERGLYSERGLNASPASNLEUTH  
 ---CHO---  
 TATCACCATGCACCGCTGAGCTGTGGACACTGGCACCTACACCTGCCAGCCATCAC (840)  
 RILETHRMETHISARGLEUGLNLEUSERASPTHRLYTHRTYRTHRCYSLNALAILETH  
 -  
 GGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCTGGTGACAGAGGAACAGTCCCAAGG (900)  
 RGLUVALASNVALTYRGLYSERGLYTHRLEUVALLEUVALTHRGLUGLUGLNSERGLNGL  
 ATGGCACAGATGCTCGGACGCCCCACCAAGGGCTCTGCCCTCCCTGCCCCACCGACAGG (960)  
 YTRPHISARGCYSSERASPALAPROPROARGALASERALEUPROALAPROPROTHRGL  
 CTCCGCCCTCCCTGACCCGACAGAGCTCTGCCCTCCCTGACCCGCCAGCAGCTCTGC (1020)  
 YSERALEUPROASPPROGLNTHRALASERALEUPROASPPROPROALAALASERAL  
 CCTCCCTGCGGCCCTGGCGGTGATCTCTCTCTCCTCGGGCTGGGCTGGGGTGGCGTG (1080)  
 ALEUPROALAALALEUALAVALILESERPHEULEULEUGLYLEUGLYLEUGLYVALALACY  
 -----TM-----\*

FIG. 8-1

TGTGCTGGCGAGGACACAGATAAAGAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGC (1140)  
 SVALLEUALAARGTHRGLNILELYSLYSLEUCYSSERTRPARGASPLYASNSERALAAL  
 -----  
 ATGTGTGGTGTACGAGGACATGTCCGACAGCCGCTGCAACACGCTGTCTCCCCCAACCA (1200)  
 ACYSVALVALTYRGLUASPMETSERHISERARGCYSASNTHRLEUSERSERPROASNGL  
 GTACCAAGTGACCCAGTGGGCCCCCTGCACGTCCCGCCTGTGGTCCCCCAACACCTTCCCT (1260)  
 NTYRGLNEND  
 GCCCCACCAATGCCCCCACCCCTGCCACACCCCTCACCTGTGTCTCTCCACGGCTGCAG (1320)  
 CAGAGTTTGAAAGGGCCCAGCGGTGCCAGCTCCAAGCAGACACACAGGCAGTGGCCAGGC (1380)  
 CCCACGGTGCTTCTCAGTGGACAATGATGCCTCCTCCGGGAAGCCTTCCCTGCCAGCCC (1440)  
 ACGCCGCCAACCGGGAGGAAGCCTGACTGTCTTTGGCTGCATCTCCCGAACATGGCCAAG (1500)  
 GAGGGCTTTTCTGTGGGATGGGCCTGGCAACGGGCCCTCTCCTGTCAAGTGGCGGCCACC (1560)  
 CACCAGCAGCCCCCAACCCCAAGGCAGCCCGGCAGAGGACGGGAGGAGACCAAGTCCCCC (1620)  
 ACCCAGCCGTACCAGAAATAAAGGCTTCTGTGCTTCAAAAAAAA (1665)  
 -----

FIG. 8-2

CCCAAATGTCAGAATGTATGTCCCAGAAACCTGTGGCTGCTTCAACCATTGACAGTTT (60)  
 METSERGLNASNVALCYSPROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL  
 -29  
 TGCTGCTGCTGGCTTCTGCAGACAGTCAAGCTGCAGCTCCCCAAAGGCTGTGCTGAAAC (120)  
 EULEULEULEUALASERALAASP SERGLNALAALAALAPROPROLYSALAVALLEULYSL  
 -1 +1  
 10 TTGAGCCCCCGTGGATCAACGTGCTCCAGGAGGACTCTGTGACTCTGACATGCCAGGGGG (180)  
 EUGLUPROPROTRPILEASNVALLEUGLNGLUASPSERVALTHRLEUTHRCYSGLNGLYA  
 \*  
 30 CTCGCAGCCCTGAGAGCGACTCCATTGAGTGGTCCACAATGGGAATCTCATTCCCACC (240)  
 LAARGSERPROGLUSERASPSERILEGLNTRPPHEHISASNGLYASNLEUILEPROTHR  
 \*  
 50 ACACGCAGCCAGCTACAGGTTCAAGGCCACAACAATGACAGCGGGAGTACAGTGCC (300)  
 ISTHRLNPROSERTYRARGPHELYSALAASNASNASPSERGLYGLUTYRTHRCYSG  
 ---CHO---  
 70 AGACTGGCCAGACCAGCCTCAGCGACCCTGTGCATCTGACTGTGCTTCCGAATGGCTGG (360)  
 LNTHRGLYGLNTHRSERLEUSERASPPROVALHISLEUTHRVALLEUSERGLUTRPLEUV  
 \*  
 90 TGCTCCAGACCCCTCACCTGGAGTTCAGGAGGGAGAAACCATCATGCTGAGGTGCCAC (420)  
 ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRILEMETLEUARGCYSHISS  
 \*  
 110 GCTGGAAGGACAAGCCTCTGGTCAAGGTCAATTCTTCCAGAATGGAAAATCCCAGAAAT (480)  
 ERTRPLYSASPLYSERLEUVALLYVALTHRPHPEGLNASNGLYLYSSERGLNLYSP  
 \*  
 130 TCTCCCGTTTGGATCCCACCTTCTCCATCCACAAGCAAACCACAGTCAAGTGGTGATT (540)  
 HESERARGLEUASPPROTHRPHESERILEPROGLNALAASNHISSEHISSEHISSEGLYASPT  
 ---CHO---  
 150 ACCACTGCAAGGAAACATAGGCTACACGCTGTTCTCATCCAAGCCTGTGACCATCACTG (600)  
 YRHISCYSTHRGLYASNILEGLYTYRTHRLEUPHESERSELYSPROVALTHRILETHR  
 \*  
 170 TCCAAGTGCCAGCATGGGAGCTCTTCAACCAATGGGGATCATTGTGGCTGTGGTCATTG (660)  
 ALGLNVALPROSERMETGLYSERSESERSESPROMETGLYILEILEVALALAVALEILEA  
 \*  
 190 CGACTGCTGTAGCAGCCATTGTTGCTGCTGTAGTGGCCTTGATCTACTGCAGGAAAAAGC (720)  
 LATHRALAVALLAALAILEVALALAALAVALVALALEUILETYRCYSARGLYSLYSA  
 TM-----  
 210 GGATTTGAGCCAAATCCACTGATCCTGTGAAGGCTGCCCAATTTGAGCCACCTGGACGTC (780)  
 RGILESERALAASNSETRASPPOVALLYSALAALAGLNPHGLUPROPROGLYARGG  
 \*  
 230 AAATGATTGCCATCAGAAAGAGACAACTGAAGAAACCAACAATGACTATGAAACAGCTG (840)  
 LNMETILEALAILEARGLYSARGGLNLEUGLUGLUTHRASNASNASPTYRGLUTHRALAA  
 \*  
 250 ACGGGCGCTACATGACTCTGAACCCAGGGCACCTACTGACGATGATAAAACATCTACC (900)  
 SPGLYGLYTYRMETTHRLEUASNPROARGALAPROTHRASPASPASPLYSASNILETYRL

FIG. 9-1



270 T G A C T C T T C C T C C C A A C G A C C A T G T C A A C A G T A A T A A C T A A A G A G T A A C G T T A T G C C A T G (960)  
 E U T H R L E U P R O P R O A S N A S P H I S V A L A S N S E R A S N A S N E N D  
 282  
 T G G T C A T A C T C T C A G C T T G C T G A G T G G A T G A C A A A A G A G G G A A T T G T T A A A G G A A A A T (1020)  
 T T A A A T G G A G A C T G G A A A A A T C C T G A G C A A A C A A A C C A C C T G G C C C T T A G A A A T A G C T T (1080)  
 T A A C T T T G C T T A A A C T A C A A A C A C A A G C A A A A C T T C A C G G G T C A T A C T A C A T A C A A G C A (1140)  
 T A A G C A A A A C T T A A C T T G G A T C A T T T C T G G T A A A T G C T T A T G T T A G A A A T A A G A C A A C C C (1200)  
 C A G C C A A T C A C A A G C A G C C T A C T A A C A T A A T T A G G T G A C T A G G G A C T T T C T A A G A A G A (1260)  
 T A C C T A C C C C C A A A A A C A A T T A T G T A A T T G A A A C C A A C C G A T T G C C T T A T T T T G C T T (1320)  
 C C A C A T T T T C C C A T A A A T A C T T G C C T G T G A C A T T T T G C C A C T G G A A C A C T A A A C T T C A T (1380)  
 G A A T T G C G C C T C A G A T T T T C C T T T A A C A T C T T T T T T T T T T G A C A G A G T C T C A A T C T G (1440)  
 T T A C C C A G G C T G G A G T G C A G T G G T G C T A T C T T G G C T C A C T G C A A C C C G C C T C C C A G G T T (1500)  
 T A A G C G A T T C T C A T G C C T C A G C C T C C C A G T A G C T G G G A T T A G A G G C A T G T G C C A T C A T A C (1560)  
 C C A G C T A A T T T T T G T A T T T T T A T T T T T T T T T T A G T A G A G A C A G G G T T T C G C A A T G T T (1620)  
 G G C C A G G C C G A T C T C G A A C T T C T G G C C T C T A G C G A T C T G C C C G C C T C G G C C T C C C A A A G T (1680)  
 G C T G G G A T G A C C A G C A T C A G C C C A A T G T C C A G C C T C T T A A C A T C T T C T T C C T A T G C C (1740)  
 C T C T C T G T G G A T C C C T A C T G C T G G T T T C T G C C T T C C A T G C T G A G A A C A A A A T C A C C T A (1800)  
 T T C A C T G C T T A T G C A G T C G G A A G C T C C A G A A G A C A A A G A G C C C A A T T A C C A G A C C A C A (1860)  
 T T A A G T C T C A T T G T T T T G C C T T G G G A T T T G A G A A G A A T T A G A G A G G T G A G G A T C T G G (1920)  
 T A T T T C C T G G A C T A A A T T C C C C T T G G G A A G A C G A A G G G A T G C T G C A G T T C C A A A A G A G A (1980)  
 A G G A C T C T T C C A G A G T C A T C T A C C T G A G T C C C A A G C T C C C T G T C C T G A A A G C C A C A G A C (2040)  
 A A T A T G G T C C C A A A T G A C T G A C T G C A C C T T C T G T G C C T C A G C C G T T C T T G A C A T C A A G A A (2100)  
 T C T T C T G T T C C A C A T C C A C A C A G C C A A T A C A A T T A G T C A A A C C A C T G T T A T T A C A G A T G (2160)  
 T A G C A A C A T G A G A A C G C T T A T G T T A C A G G T T A C A T G A G A G C A A T C A T G T A A G T C T A T A T (2220)  
 G A C T T C A G A A A T G T T A A A A T A G A C T A A C C T C T A A C A A C A A A T T A A A A G T G A T T G T T T C A A (2280)  
 G G T G A A A A A A (2290)

FIG. 9-2

```

1  AAAGACAAACTGCACCCACTGAACTCCGCAGCTAGCATCCAAATCAGCCCTTGAGATTTGAGGCCTTGGAGACTCAGGAGTTTGTGAGAGC
91  AAAATGACAACACCCAGAAATTCAGTAAATGGGACTTTCCCGGCAGAGCCCAATGAAAGGCCCTATTGCTATGCAATCTGGTCCAAAAACCA
1  Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro
    ---CHO---
181 CTCTTCAGGAGGATGTCCTTCACTGGTGGGCCCCCAGCAAGCTTCTTCAATGAGGGAATCTAAGACTTTGGGGGCTGTCCAGATTATGAAT
30  Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn
    =====
271 GGGCTCTTCCACATTGCCCTGGGGGTCTCTGATGATCCAGCAGGATCTATGCACCCATCIGTGTGACTGTGTGGTACCCCTCTCTCTGG
60  Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp
    =====
361 GGAGGCATTATGTATATATTTCGGGATCCTCTGGCAGCAACGAGAAAAAATCCAGGAAGTGTTTGGTCAAAGGAAAAAATGATAATG
90  Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met
    =====
451 AATTCATTGAGCCCTCTTTGCTGCCATTTCTGGAATGATCTTTCAATCATGGACATACTTAATATTAAAAATTTCCCATTTTAAAAAATG
120 Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met
    =====
441 GAGAGTCTGAATTTTATTAGAGCTCACACACCATATATATTAAACATATACAACCTGTGAACCCAGCTAAATCCCTCTGAGAAAAAACTCCCCATC
150 Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
    =====
631 ACCCAATACTGTTACAGCATACAATCTCTGTTCTTGGGCATTTTGTGAGTGATGCTGATCTTTTGCCTTCTTCCAGGAACCTTGTAATAGCT
180 Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala
    =====

```

FIG. 10A-1

721 GGCATCGTTGAGAAATGAATGGAAAAGAACGTGCTCCAGACCCAAATCTAACATAGTTCTCTGTCTCAGCAGAGAAGAAAAAGAACAGACT  
 210 GlyIleValGluAsnGluTrpLysArgThrCysSerArgProLysSerAsnIleValLeuLeuSerAlaGluGluLysLysGluGlnThr

811 ATTGAAATAAAAGAAGAAGTGGTTGGGCTAACTGAAACATCTTCCCAACCAAGAATGAAGAAGACATTGAATAATTATCCAAATCCAAGAA  
 240 IleGluIleLysGluGluValValGlyLeuThrSerSerGlnProLysAsnGluGluAspIleGluIleIleProIleGlnGlu

901 GAGGAAGAAGAAGAACAGAGACGAACCTTCCAGAACCTCCCAAGATCAGGAATCCTCACCAATAGAAAATGACAGCTCTCCTTAAGTG  
 270 GluGluGluGluThrGluThrGluThrAsnPheProGluProGluSerSerProIleGluAsnAspSerSerProEnd 297  
 ---CHD---

991 ATTTCTTCTGTTTTCTGTTCCTTTTTTAAACATTAGTGTTCATAGCTTCCAAGAGACATGCTGACTTTTCAATTTCTTGAGGTACTCTGCA  
 \*

1081 CATACGCCACCACATCTCTATCTGGCCTTTGCAATGGAGTGACCATAGCTCCTTCTCTTACATTGAATGTAGAGAATGTAGCCATTGTAG

1171 CAGCTTGTTGTCACGCTTCTCTTTTGAGCAACTTTCTTACACTGAAGAAGGCAGAATGAGTGCTTCAGAATGTGATTTTCCTACTAA

1261 CCTGTTCTTGGATAGGCTTTTTTAGTATAGTATTTTTTTTGTGTCATTTTCTCCATCAGCAACCAGGGAGACTGCACCTGATGGAAAAGAT

1351 ATATGACTGCTTCATGACATTCTCTAAACTATCTTTTTTTTATCCACATCTACGTTTTTGGTGGAGTCCCCTTTTATCATCTCTTAAACA

1441 ATGATGCAAAAGGGCTTTAGAGCACAATGGATCT 1474

FIG. 10A-2

FOOT-HSEB

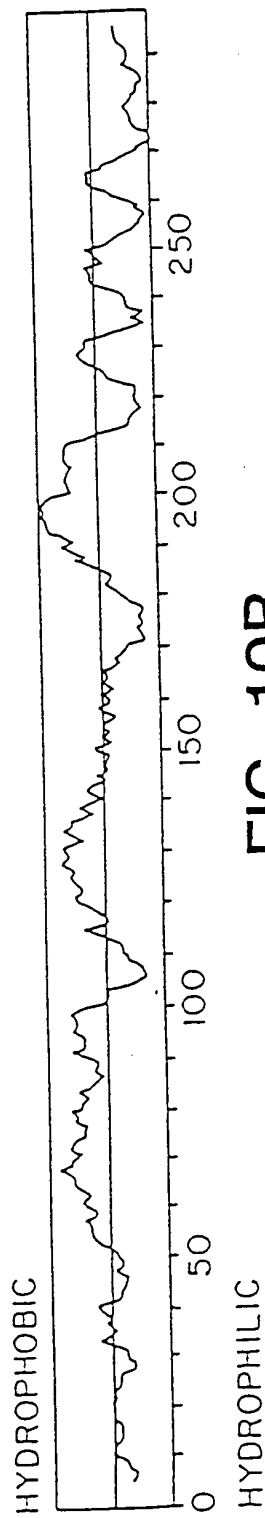


FIG. 10B

1 CTCAGCCTCGCTATGGCTCCAGCAGCCCCCGCGCTGCGCCGCACTCCTGGTCCTGCTCGGGGCTCTGTCCCA  
 MetAlaProSerSerProArgProAlaLeuProAlaLeuLeuValLeuLeuGlyAlaLeuPhePro  
 (-25)  
 GGACCTGGCAATGCCCCAGACATCTGTGTCCCTCAAAAGTC  
 GlyProGlyAsnAlaGlnThrSerValSerProSerLysVal  
 (+11)  
 121 ATCCTGCCCCGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGGCATAGAGACC  
 IleLeuProArgGlyGlySerValLeuValThrCysSerThrSerCysAspGlnProLysLeuLeuGlyIleGluThr  
 (+1)  
 CCGTTGCCCTAAAGAGTTGCTCCTGCCTGGGAACAACCGG  
 ProLeuProLysLysGluLeuLeuLeuProGlyAsnAsnArg  
 (+81)  
 241 AAGGTGTATGAAGCAATGTGCAAGAAGATAGCCAAECCTGTGCTATTCAAACTGCCCTGATGGGCAGTCAACA  
 LysValTyrGluLeuSerAsnValGlnGluAspSerGlnProMetCysTyrSerAsnCysProAspGlyGlnSerThr  
 GCTAAACCTTCCTCACCGTGTACTGGACTCCAGAACGGGTG  
 AlaLysThrPheLeuThrValTyrTrpThrProGluArgVal  
 (+91)  
 361 GAACTGGCACCCCTCCCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGCACCC  
 GluLeuAlaProLeuProSerTrpGlnProValGlyLysAsnLeuThrLeuArgCysGlnValGluGlyGlyAlaPro  
 ----CHO----  
 CGGGCCAAACCTCACCGTGGTGTCTCCGTGGGGAGAAGGAG  
 ArgAlaAsnLeuThrValValLeuLeuArgGlyGluLysGlu  
 -----(+131)  
 481 CTGAAACGGGAGCCAGCTGTGGGGAGCCCCGCTGAGGTACGACACCGGTGCTGTGAGGAGATCACCATGGAGCC  
 LeuLysArgGluProAlaValGlyGluProAlaGluValThrThrValLeuValArgArgAspHisGlyAla  
 AATTTCTGTGCGCGCACTGAACCTGGACCTGCGGCCCCCAAGGG  
 AsnPheSerCysArgThrGluLeuAspLeuArgProGlnGly  
 ----CHO----(+171)  
 801 CTGGAGCTGTTTGAGAACACCTCGGCCCTTACCAGCTCCAGACCTTTGTCTGCCAGCGACTCCCCCACAACCTTGTC  
 LeuGluLeuPheGluAsnThrSerAlaProTyrGlnLeuGlnThrPheValLeuProAlaThrProProGlnLeuVal  
 ----CHO----  
 AGCCCCCGGTCCTAGAGGTGGACACGCGAGGGACCGCTGGTC  
 SerProArgValLeuGluValAspThrGlnGlyThrValVal  
 (+211)

FIG. 11-1

721 TGTTCCTGGACGGGCTGTTCCAGTCTCGGAGGCCAGGTCCACCTGGCACTGGGGGACCAGAGGTGAAACCCACA  
CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr  
GTCACCTATGGCAACGACTCCTTCTCGGCCAAGGCCCTCAGTC  
ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal  
(+251)  
---CHO---

841 AGTGTGACCGCAGAGGACGAGGGCACCCAGCGGCTGACGTGTGCAGTAATACTGGGGAACCCAGAGCCAGGAGACACTG  
SerValThrAlaGluAspGluGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu  
---CHO---

CAGACAGTGACCATCTACAGCTTTCCGGCGCCCAACGTGATT  
GlnThrValThrIleTyrSerPheProAlaProAsnValIle  
(+291)

961 CTGACGAAGCCAGAGGTCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCCACCCCTAGAGCCAAGGTGACGCTG  
LeuThrLysProGluValSerGluGlyThrGluValThrValLysCysGluAlaHisProArgAlaLysValThrLeu  
AATGGGGTTCCAGCCCGCCACTGGGCCCGAGGGCCCCAGCTC  
AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu  
(+331)

1081 CTGCTGAAGCCACCCAGAGGACAACGGGCGCAGCTTCTCCTGCTCTGCAACCCCTGGAGGTGGCCCGCCAGCTTATA  
LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle  
CACAAAGAACCAAGACCCGGGAGCTTCGTGCTCCTGTATGGCCCC  
HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro  
(+371)  
---CHO---

1201 CGACTGGACGAGAGGGATTGTCCGGGAAACTGGACGTGGCCAGAAATTTCCAGCAGACTCCAATGTGCCAGGCTTGG  
ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnGlnThrProMetCysGlnAlaTrp  
---CHO---

GGGAACCCATTGCCCCGAGCTCAAGTGTCTAAAGGATGGCACT  
GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr  
(+411)

1321 TTCCCACTGCCCCATCGGGGAATCAGTGACTGTCACTCGAGATCTTGAGGGGCACCTACCTCTGTCCGGCCAGGAGCACT  
PheProLeuProIleGlyGluSerValThrValThrArgAspLeuGluGlyThrTyrLeuCysArgAlaArgSerThr  
CAAGGGGAGGTCAACCCCGGAGGTGACCGTGAATGTGCTCTCC  
GlnGlyGluValThrArgGluValThrValAsnValLeuSer  
(+451)

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1441 CCCCCGTATGAGATTGTCATCATCACTGTGGTAGCAGCGCCAGTCATAATGGGCACTGCAGGCCCTCAGCACGTACCTC
ProArgTyrGluIleValIleIleThrValValAlaAlaValIleMetGlyThrAlaGlyLeuSerThrTyrLeu
-----TM-----
TATAACCGCCAGCGGAAGATCAAGAAATACAGACTACAACAG
TyrAsnArgGlnArgLysIleLysLysTyrArgLeuGlnGln
(+491)
1561 GCCCCAAAAGGGACCCCCCATGAAACCGAACACACAAAGCCCTCCCTGAACCTATCCCCGGACAGGGCCTCTTCCT
AlaGlnLysGlyThrProMetLysProAsnThrGlnAlaThrProPro
(+507)
CGGCCCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACAGA

1681 GTGGAAGACATATGCCATGCAGCTACACCTACCGGCCCTGGGACGCCGGAGGACAGGGCATTGTCCTCAGTCAGATAC
1801 GGCCACGCATCTGATCTGTAGTCACATGACTAAGCCAAGAGGAAG
AACAGCATTGGGGCCCATGGTACCTGCACACACCTAAACACTA

```

FIG. 11-3

0936544-043701

1 ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT  
51 CTTCTCACC CCCATGGAAG TCAGGCCCCG GGAACCTCTA GTGGTGAAGG  
101 TGGAGAGGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT  
151 GGCCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCTT  
201 CTAAAACTC AGCCTGGGGC TGCCAGGCCT GGGAATCCAC ATGAGGCCCC  
251 TGGcCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC  
301 TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG  
351 GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG  
401 ACCTAGGTGG CCTGGGCTGT GGCCTGAAGA ACAGGTCCTC AGAGGGCCCC  
451 AGCTCCCCCT CCGGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA  
501 AGACCGCCCT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG  
551 ACAGCCTGAA CAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC  
601 AACTCTGGC TGTCCTGTGG GGTACCCCT GACTCTGTGT CCAGGGGCCC  
651 CCTCTCCTGG ACCCATGTGC ACCCAAGGG GCCTAAGTCA TTGCTGAGCC  
701 TAGAGCTGAA GGACGATCGC CCGCCAGAG ATATGTGGGT AATGGAGACG  
751 GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGGA AGTATTATTG  
801 TCACCGTGGC AACCTGACCA TGTCATTCCA CCTGGAGATC ACTGCTCGGC  
851 CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT  
901 GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTCCCTTG TGGGCATTCT  
951 TCATCTTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG  
1001 ACCCCACCAG GAGATTCTTC AAAGTGACGC CTCCCCCAGG AAGCGGGCCC  
1051 CAGAACCAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT  
1101 CGGACGCGCC CAGCGTTGGG CCGCAGGCCT GGGGGGCACT GCCCCGTCTT  
1151 ATGGAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGGTCCCCG

FIG. 12-1



0936544-041701

1201 AGCCGCCGGG AGTGGGCCCA GAAGAAGAGG AAGGGGAGGG CTATGAGGAA  
1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG  
1301 GCAGGACCAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG  
1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT  
1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTCGCCAGGA CAATGGACTT  
1451 CCTGAGCCCT CATGGGTCAG CCTGGGACCC CAGCCGGGAA GCAACCTCCC  
1501 TGGGGTCCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC  
1551 CAGCTCCGCT CCATTCCGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC  
1601 AGACTCTTAT GAGAACATGG ATAATCCCGA TGGGCCAGAC CCAGCCTGGG  
1651 GAGGAGGGGG CCGCATGGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC  
1701 CAGCCTGGAT CTCCTCAAGT CCCCAGATT CACACCTGAC TCTGAAATCT  
1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT  
1801 GTGTGCATGT GTGTAAGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT  
1851 ATACATGCCA GTGACACTTC CAGTCCCCTT TGTATTCCTT AAATAAACTC  
1901 AATGAGCTCT TCCAAAAAAA AAAA

FIG. 12-2

0936544.043701

1 ACAAAGACAA ACTGCACCCA CTGAACTCCG CAGCTAGCAT CCAAATCAGC  
51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTTGAGA GCAAAATGAC  
101 AACACCCAGA AATTCAGTAA ATGGGACTTT CCCGCCAGAG CCAATGAAAG  
151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT  
201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT  
251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC  
301 TTCTGATGAT CCCAGCAGGG ATCTATGCAC CCATCTGTGT GACTGTGTGG  
351 TACCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC  
401 AGCAACGGAG AAAAATCCA GGAAGTGTTC GGTCAAAGGA AAAATGATAA  
451 TGAATTCATT GAGCCTCTTT GCTGCCATTT CTGGAATGAT TCTTTCAATC  
501 ATGGACATAC TTAATATTAA AATTTCCCAT TTTTAAAAA TGGAGAGTCT  
551 GAATTTTATT AGAGCTCACA CACCATATAT TAACATATAC AACTGTGAAC  
601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC  
651 ATACAATCTC TGTTCTTGGG CATTTTGTC A GTGATGCTGA TCTTTGCCTT  
701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA  
751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA  
801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGGC TAACTGAAAC  
851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG  
901 AAGAGGAAGA AGAAGAAACA GAGACGAACT TTCCAGAACC TCCCCAAGAT  
951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC  
1001 TGTTCCTGT TTCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC  
1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

FIG. 13-1

0936544-041701

1101 ATCTGGCCTT TGCATGGAGT GACCATAGCT CCTTCTCTCT TACATTGAAT  
1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTACAGC TTCTTCTTTT  
1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG  
1251 ATTCCTACT AACCTGTTCC TTGGATAGGC TTTTITAGTAT AGTATTTTTT  
1301 TTTGTCATTI TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG  
1351 ATATATGACT GCTTCATGAC ATTCCTAAAC TATCTTTTTT TTATTCCACA  
1401 TCTACGTTTT TGGTGGAGTC CCTTTTTATC ATCCTTAAAA CAATGATGCA  
1451 AAAGGGCTTT AGAGCACAAT GGATCT

FIG. 13-2

1 CCCAAATGTC TCAGAATGTA TGTCCCAGAA ACCTGTGGCT GCTTCAACCA  
 51 TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC  
 101 CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG  
 151 AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGCGAC  
 201 TCCATTCACT GGTTCACAA TGGGAATCTC ATTCCCACCC ACACGCAGCC  
 251 CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC  
 301 AGACTGGCCA GACCAGCCTC AGCGACCCTG TGCATCTGAC TGTGCTTTCC  
 351 GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTTCAGG AGGGAGAAAC  
 401 CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA  
 451 CATTCTTCCA GAATGGAAAA TCCCAGAAAT TCTCCCGTTT GGATCCCACC  
 501 TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC  
 551 AGGAAACATA GGCTACACGC TGTTCATC CAAGCCTGTG ACCATCACTG  
 601 TCCAAGTGCC CAGCATGGGC AGCTCTTCAC CAATGGGGAT CATTGTGGCT  
 651 GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT  
 701 GATCTACTGC AGGAAAAAGC GGATTTTCAGC CAATTCCACT GATCCTGTGA  
 751 AGGCTGCCCC ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG  
 801 AGACAACTTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCGGCTA  
 851 CATGACTCTG AACCCCAGGG CACCTACTGA CGATGATAAA AACATCTACC  
 901 TGAATCTTCC TCCCAACGAC CATGTCAACA GTAATAACTA AAGAGTAACG  
 951 TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG AAAAAAGAG  
 1001 GGGAAATTGTT AAAGGAAAAT TAAATGGAG ACTGGAAAAA TCCTGAGCAA  
 1051 ACAAACCAC CTGGCCCTTA GAAATAGCTT TAACTTTGCT TAACTACAA  
 1101 ACACAAGCAA AACTTCACGG GGTCACTA CATAAGCA TAAGCAAAAC  
 1151 TTAATTGGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC  
 1201 CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT  
 1251 TCTAAGAAGA TACCTACCCC CAAAAACAA TTATGTAATT GAAAACCAAC  
 1301 CGATTGCCTT TATTTTGCTT CCACATTTTC CCAATAAATA CTTGCCTGTG  
 1351 ACATTTTGCC ACTGGAACAC TAACTTCAT GAATTGCGCC TCAGATTTTT  
 1401 CCTTTAACAT CTTTTTTTTT TTTGACAGAG TCTCAATCTG TTACCCAGGC  
 1451 TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGT  
 1501 TAAGCGATTG TCATGCCTCA GCCTCCCAGT AGCTGGGATT AGAGGCATGT  
 1551 GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTTT TTTTGTAGT  
 1601 AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT  
 1651 AGCGATCTGC CCGCCTCGGC CTCCCAAAGT GCTGGGATGA CCAGCATCAG

FIG. 15-1

00036544.041701

1701 CCCCATGTC CAGCCTCTTT AACATCTTCT TTCCTATGCC CTCTCTGTGG  
1751 ATCCCTACTG CTGGTTTCTG CTTTCTCCAT GCTGAGAACA AAATCACCTA  
1801 TTCCTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAGA GCCCAATTAC  
1851 CAGAACCACA TTAAGTCTCC ATTGTTTTGC CTTGGGATTT GAGAAGAGAA  
1901 TTAGAGAGGT GAGGATCTGG TATTTCTGG ACTAAATTCC CCTTGGGGAA  
1951 GACGAAGGGA TGCTGCAGTT CCAAAAGAGA AGGACTCTTC CAGAGTCATC  
2001 TACCTGAGTC CCAAAGCTCC CTGTCCTGAA AGCCACAGAC AATATGGTCC  
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTTG ACATCAAGAA  
2101 TCTTCTGTT CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA  
2151 TTAACAGATG TAGCAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA  
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAAT AGACTAACCT  
2251 CTAACAACAA ATTAAGAGTG ATTGTTTCAA GGTGAAAAAA

FIG. 15-2

09836544.041701

1 GCTGTGACTG CTGTGCTCTG GCGGCCACTC GCTCCAGGGA GTGATGGGAA  
51 TCCTGTCATT CTTACCTGTC CTTGCCACTG AGAGTGA CTG GCTGACTGC  
101 AAGTCCCCC AGCCTTGGG TCATATGCTT CTGTGGACAG CTGTGCTATC  
151 CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCAAAG GCTGTGCTGA  
201 AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG  
251 ACATGCCGGG GGA CTACAG CCCTGAGAGC GACTCCATTG AGTGGTTCCA  
301 CAATGGGAAT CTCATTCCCA CCCACACGCA GCCAGCTAC AGGTTCAAGG  
351 CCAACAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC  
401 CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC  
451 CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA  
501 GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG  
551 AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCCTCAGT TCTGATTGAA  
601 CAGAAGAAGG TTTCAAGGCC AAAACAGGC AGCCAAGTGT GAGAGAAGCA  
651 GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTTAA TGGCAGAATT  
701 GAAAAGCACA GACCACA ACT GAATCCTAGC CCTGGAAATG ACTCACTATA  
751 CAACATGATG AATTCATTTA ACCCTTGAGT TTCCATTCTC TCACCTGCTC  
801 CGTGGGGCAG TAACGCCTCC CTCAGAGGCT TCTGGTGAGA ATCAGTGTTT  
851 CCCTGCCCCC GCCCCGCCCT CCATGCCCTC TCTCCACGTT CTCACTGTGC  
901 TAGGTGCTCT TCTCTGTCTT TCTCTTCCAC CAGCCTGTGG GAAACCTGAG  
951 ATGAAAGTCG TGCTTACCC ATCTTTGTAT TTCCAGCATC TGAAACTGGG  
1001 CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC  
1051 CCATTGAAAG GTGGCTCTCT GTAAAGCAA GTTACAATGA GATTGTGATG  
1101 AACATTGTCC TTGTGGCTTT TCACTTAGTC CCCTCCCTTC ACCTGAAGAG  
1151 CAAATTTTCC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT  
1201 GTTGCCTTTA GACCCTGCTG GAAAGAAGCT CCACATTTAT TAACATTCCC  
1251 GAAGTAAATT TATCAGGTAG CATTATCAG GTAACATTTG TTGCACATTC  
1301 ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCCTTATCA TATGCCGACT  
1351 CCTCGGTCAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC  
1401 ATCTTAGGGT CTCTTGTTT CTTCTGCAG AGGCCTGTG GGCAGGAAAA  
1451 GGCTGCAGCT GCCTTCCCTG GAGAAGGAGG AGATGAGTGT ATCCTGAACA  
1501 CCTATTATGT GCTAGGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT  
1551 TTTCACGAAT GAGGAACTG AGGCTCAGAA GACTTAAATT ATTTGCCCAA  
1601 GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTICA  
1651 GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCAGTA AGGAAGATCT

FIG. 16-1

09836544.041701

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCTCTGCG GTTTTTTGTG  
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG  
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC  
1851 AAGGTCACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTCGGA  
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC  
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC  
2001 ATCACTGTCC AAGCTCCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT  
2051 GGTCACGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA  
2101 TCTACTGCAG GAAAAAGCGG ATTTCAAGTT TGTAGCTCCT CCCGGTCCCT  
2151 TTTGTTATCA GTTCCACTT T

FIG. 16-2

0936544.043701

1 GCCTCGCTCG GCGGCCAGT GGTCTGCCG CCTGGTCTCA CCTCGCCATG  
51 GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT  
101 CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACA  
151 GTCAGTGCTG TTCTTTGTGC CAGCCAGGAC AGAAACTGGT GAGTGA CTGC  
201 ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA GCGAATTCCT  
251 AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC  
301 CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC  
351 ATCTGCACCT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG  
401 CTGTGTCCTG CACCGCTCAT GCTCGCCCGG CTTTGGGGTC AAGCAGATTG  
451 CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCCAGT CGGCTTCTTC  
501 TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGGA CAAGCTGTGA  
551 GACCAAAGAC CTGGTTGTGC AACAGGCAGGC ACAAACAAGA CTGATGTTGT  
601 CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT  
651 TCGGGATCCT GTTTGCCATC CTCTTGGTGC TGGTCTTTAT CAAAAAGGTG  
701 GCCAAGAAGC CAACCAATAA GGCCCCCAC CCCAAGCAGG AACCCAGGA  
751 GATCAATTTT CCCGACGATC TTCCTGGCTC CAACACTGCT GCTCCAGTGC  
801 AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG  
851 AGTCGCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT  
901 GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC  
951 TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCACTCA GTGCCAGCCC  
CTC

FIG. 17